

expanded to determine the expression of hundreds or thousands of genes simultaneously (e.g. by DNA arrays). We can create hypotheses which state that expression of a single specific gene can be used to determine the potential of a culture, or hypotheses that state that the expression of a group of genes (e.g., hypothetical genes A, B, C, D, E, F) acts as an indicator of high embryonic potential. For example, all these genes may be expressed at a high level in cell lines that produce large numbers of embryos, thus we would select cell lines which exhibited this characteristic. Alternatively specific levels of expression for genes A, B, C, D, E and F may be required and a combination of high and low expression of particular genes will identify desirable cultures. Alternatively, experience will determine that certain exceptions can be tolerated.

[0182] While the previous paragraphs discuss numbers of embryos produced, the principle applies to ANY desired characteristic: by establishing a correlation of gene expression with e.g., germination potential, embryo size, growth of plantlets in their first year, disease resistance of mature plants, environmental hardiness or wood quality. Any trait where could be evaluated by these gene expression assays and correlations with gene expression established, resulting in a molecular tool which could be used to predict desirable characteristics. Explicitly, we could use these gene expression tools to select cell lines which will produce high quality plantlets months before they grow into plantlets, or cell lines or juvenile plantlets which will produce hardy trees with desirable wood quality, years before these traits are expressed.

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TABLE I

| cDNA        | Embryo Phase | Clone   | Nucleotide Sequence  |
|-------------|--------------|---------|--|
| SEQ ID NO:1 | Late         | LPS-001 | GGTACTCCACCGTAATAACCCCTTGGGAAATAGCCTATGATCCAGGGGAGGCAACC<br>ACCTATATCATTGACAACAGCGAAAAATGTGGCGCAAGAAGTTTCACATACAATTCA<br>TGGTTACAAAGATCACATACCAGGTGTTGGAGCAGATTGATAGATATTGAAGATAT<br>GAAGCCAAGGAGTGGAGCAGTTATTGAAAAGGGCACAAAAAATTTGCCATTTACA<br>AAGATGAAAAATGGGCTGATTCACAAATACTCGGCAATATGCCACACATGAAGTGT<br>ATTGTGAAATGGAATCCTATAGACTCAACTTTTCGATTGCCCTGCCATGGTTCAATG<br>TTTGATAATCTGGGTCGATGCATCAATGGACCTGCCAAGGCGGACCTATTTCCCGA<br>AGATTACGATAGTTGTTTGTACATGTAATTATCTTGATATTGTATATATATGATTTA<br>AATTATACAGTACAATAAATCCATGTTTGCAGGCTATTTCTGCTTGATAATTTAGCTC<br>CAGATTTATACATAACCAGTTTATTTGGCTGTTTTTCCCCTGGCAAAAAAAAAAAAA                  |
| SEQ ID NO:2 | Late         | LPS-003 | 003GGTACTCCACAGAAAGAAATGATTTGACAGAAAAAGAGAGCTGTAGGATTGGGT<br>AAACCCCTGCAGTGATATATACAATGTATATGACTCTGTCTGTTTTCTGTTATTTG<br>ACGGAAATAAAACGCCATAGCGACGGATGACTGTAATCCTTAGGGACGGATGAC<br>TGTAATCCTTAGGTTGGAAGATTACAAACGACATATGGGCTTTCAATTTTCAGAT<br>TTCTGTAAGACTTACATTTCAAAGACTGTTTGGATGGGCAAAAAAAAAAAAA   |
| SEQ ID NO:3 | Middle       | LPS-004 | GGTACTCCACCAGAATGCCGCAGTTTAGTTCTCTAAAGCAAGCAGTAAATTAATTTT<br>GTCAAAATCTAAGAGTGTATAGTATCAGTGGGTTTGTATTTCTAGTTTGCCCTACA<br>ATAACGATGGGGATTACCAGTTTTTGTAGAATTTGCAATCATCGGATGACAAATTC<br>AAAGTTTTCTTAAGTCAACCCGCAATTGATATCGAGAAGCCTTCCATTTTCAATTATT<br>AATATCAGAAAATCTTTTCAGTTGGCAAAAAAAAAAAAA   |
| SEQ ID NO:4 | Middle       | LPS-006 | AGCCAGCTGCCAAGGGGATGTGCTGCAAGCGATAAGTGGTAACGCCAGGTTTCC<br>AGTCAGACGTGTAACGACGCCAGTGATGTATACGAATCACTATAGCGATGGCCT<br>TCTAGATGCATGCTCGAGCGCCGCAAGTGTGATGAATTGCAGAATCGGCTGGTACT<br>CACGGGCTAGAGAAAGGCACAAGCACTTTTTGTCATTTTAGGATCAGAGGCATTCA<br>GGTATAGGAAGGGTGGCTCAGATAGGCAGATGGATCGGCATTTTGCCAGTCATG<br>AAACATTTTATGCATGTTATTGCCTCCCAAGGACGAAATCAGTTCTTTGTGCCCTTCT<br>GGTGATCACTTCAAACAAAAGGCAACAGTTCTGTGATTTCATATGGTTTGTCACT<br>GAATATTTTGTGCAGATGTTCTCTACTATTTTATCTGCTTCAAGTGATTATTTG<br>TTGATCCCCATGGATAGTTATGCTAATCAGTTGCATTCTCTTGACCAGTCAACA<br>AACAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGTAAACGTGTAG<br>CTAATTGTTCTGGCAAAAAAAAAAAAA |
| SEQ ID NO:5 | Middle       | LPS-007 | TCCAAAATACAAAGGCTTTATTTGCATCATGATATAATACAAAGTAAGAAATTTACCC<br>AACTGTTTAACCTAATAATAACAAAGGAAGCATTTTACCCTACTTTAACGTAAT<br>AATACCAAAGAGTGGAATGCTTTATTGACCAGCAAGACCTTGAAATTTTATAACCA<br>ATGCCCATCAACAGAGCCTTTCTTAAAAAACGCAAGGCCAGCTCTGTCACCTTATT<br>AGTTAGTATAAACTGACATTCCTTCAAGCTTGTGTGCGCAGAAACAATAAAGAACTT<br>CACCTTGGTTTAAAGAACGTGCCATGAAGAAAACGTCCCAAGAAAAATGAAATGGC<br>TCCTTCGACCATTCAGTCCTCCCTAGAAAAATCAAAGACTCCTTCGACCATTAGGT<br>CCTCCAATTGGGCATCTAATACAAGCGGTC  |
| SEQ ID NO:6 | Middle       | LPS-008 | GGTACTCCACGGGCTAGAGAAAAGGCACAAGCACTTCTTCGTCATTTTAGGGATCA<br>GAGGCATTCAGGTATAGGAAGGGTGGCTCAGATAGGCAGATGGATCGGCATTTT<br>GCCAGTCATGAAACATTTTATGCATGTTATTGCCTCCCAAGGACGAAATCAGTTCT<br>TTGTGCCCTTCTGGTGATATCACTTCAAACAAAAGGCAACAGTTCTGTGATTTCATAT<br>GGTTTGTCACTGAATATTTTGTGCAGATGTTCTCTACTATTTTATCTGCTTCAA<br>GTGATTATTTGTTGATTCCCATGGATAGTTATGCTAATCAGTTGCATTCTCTTGTA<br>CCAGTCAACAACAAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGT<br>AAACGTGTAGCTAATTGTTCTGGCAAAAAAAAAAAAA  |

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| cDNA         | Embryo Phase | Clone   | Nucleotide Sequence   |
|--------------|--------------|---------|---|
| SEQ ID NO:7  | Middle       | LPS-010 | ACGACGTGTAAACGACGGCCAGTGATTGTATACGACTCACTATAGGGCGATTGGC<br>CTTCTAGATGCATGCTCGAGCGGCCGAGGTGATGGATATCTGCAGAATTCGCTT<br>GGTACTCCACGGCTAGAGAAAAGGCACAAGCACTTCTTCGTCATTTTAGGATCAGA<br>GGCATTCAAGGTATAGGAAGGGTGGTCAGATAGGCAGATGGATCGGCATTTGCC<br>AGTCATGAAACATTTTATGCATGTTATTGCCCTCCCAAGGACGAAATCAGTCTTTGT<br>GCCTTCTGGTGATATCACTTCAAACAAAAGGCAACAGTCTGTGATTTCATATGGTT<br>TGCTACTGAATATTTTGTTCAGATGTTCTCTACTATTTTATCTGCTTCAAGTGA<br>TTATTTGTTGATTCCCATGGATAGTTATGCTAATCAGTTGCATTCTCTTGATACCAG<br>TCAACAAACAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGTAAAC<br>GTGTAGCTAATTGTTCTGGCAAAAAAAAAAAAA  |
| SEQ ID NO:8  | Middle       | LPS-011 | GGTACTCCACGAAGCAAAAAGAGTCAGGGGAATGAAGATGGGGGGCTCCGACAAG<br>AAGCGGATCAGAGAAGAGCAGGAAATGAGTCCACCTGAGGAATCCTGGAGACAGA<br>AACAGGGGGCGTTTAAATGGAGTTTGAGGCAGGGATGGCCTATGATAAACCTGAAAT<br>GCCGGTGCAGGTAATGAGAATTTGCCAGAGTTTGTCTCTTTCAAATGAGTACTC<br>GATGTTATTGAAAGATCCATGGAGTTGGGAGGATAGCACTGGTTTCGGAATCCGAA<br>GCTTAGCTGCTGTGAGGAAGCAGTCTTGATATTGGACTATCTCCATGATTCTGCT<br>GTAGATAATCGCTGTGAAAAGGATTTGCCGAGCAGCACAAGGTACAGGAAGAGG<br>AGGATTGTTTGAGAAGGTCTCTTTTGAAGCCACAGATGATCAGCTCTGGAGGCTT<br>CAGAGTCTTTGCAGGATACAGAAGGTCTGTTTCCTCTGGATTCCGTGGGTAGCCAT<br>GATTGCACGACCTTGTTCAGGATGAGAGCATTGTTCAAGGGCGCTGCTTCTACTT<br>CAGAATTTGGGAACAGGATGATGGTCACAAGGATGCCAAAATCATGAAGATGGCA<br>TTGTTTTGTGTATGGGAGTGGGATCTCGGATTGGATTCCGAGGCTCCCTCGAA<br>TCAATCTGAGTTTTCTGAATCTGTTGAATTTGAAAGCTCTATGTTTTCACTGAATTT<br>GGGTCTTTTAATTTCTTCTATGAATTTGGGTGTTTCTAATTTCTTCTTCAGCAA<br>AAAAAAAAAAAA |
| SEQ ID NO:9  | Middle       | LPS-012 | GGTACTCCACCATATCCAGGTAAACAAGGGAAAACAGAGTCAGCTTCTAGTATGTT<br>GTATGCCCTGCTCTGTCTGTTTTCTTTGATCTTTGATGCCAAGCAAGTTGAATGTGA<br>TCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTGTCTCTTTGGTGTCTATTA<br>GCACAGAAGCTATTGGAGAAATGATTATTATCTGTTTGATAACTTCTAGAGCATTTT<br>TCTGCTTCCAATTCACAAGGTGGAAGTGCAAGGATGTTTACTTTCTTAACTGTA<br>CTTGCTTGATTTGATGATGTAAGGTTGTGTGGCAAAAAAAAAAAAA   |
| SEQ ID NO:10 | Middle       | LPS-013 | GGTACTCACCATATCCGGTAACAAGGGAACAAGTCAGTTTTAGAAAGTGGACCCCC<br>GGTTCGCTCGTTTTCTTGATCTCGGAGCCAAGCAAGTGATGTGATCACTAAATGT<br>TGCTGGCAGTAGAGCTGGAGATGTGCTGTCTTTGGGTCAATAGCACAGAAGCTA<br>TTGGAGAAATGATTATGGTATTCACCATATCCAGGTAACAAGGGAAAACAGAGC<br>TCAGCTTCTAGTATGTTGTATGCCCTGCTCTGTCTGTTTTCTTTGATCTTTGATGCC<br>AAGCAAGTTGAATGTGATCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTG<br>TCTCTTTGGTGTCAATAGCACAGAAGCTATTGGAGAAATGATTATTATCTGTTTGAT<br>AACTTCTAGAGCATTTTTCTGCTTCCAATTCACAAGGTGGAAGTGCAAGGATGTT<br>TACTTTCTTAACTGTACTTGCCTTGATTTGATGATGTAAGGTTGTGTGGCAAAAA<br>AAAAAA   |
| SEQ ID NO:11 | Middle       | LPS-014 | GGTACTCACCATATCCATGTAAACAAGGGAAAACAGAGCTCAGCTTCTAGTATGT<br>AGTATGCCCTGCTCTGTCTGTTTTCTTTGATCTTTGATGCCAAGCAAGTTGAATGTG<br>ATCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTGTCTCTTTGGTGTCAAT<br>AGCACAGAAGCTATTGGAGAAATGATTATTATCTGTTACATAACTTATAGAGCATTTT<br>TCTGCTTCCAATTCACAAGGTGGAAGTGCAAGGATGTTTACTTTCTTAACTGTA<br>CTTGCTTGATTTGATGATGTAAGGTTGTGTGGCAAAAAAAAAAAAA  |
| SEQ ID NO:12 | Late         | LPS-015 | GGTACTCCACTAGACCGGGTAGGGTCTCTCCATGGTTTTGCGACTTAGGTTAGGTG<br>TCCTGTTCTGTTAATGATTTTGAGGTTTTGTAATTGTGAGTATGTTTCCAGGGTTTT<br>GAACCTGGGTACTCGGCCCTTTGTTGGAATGTAGTCTGGTTAATTTATATGATATGT<br>AACCTTGGGGTTTCGAGCCAGTCTCTGTTCTTCTTGAATGAAATGCGATTGTT<br>CTAAAAAAAAAAAA   |

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